

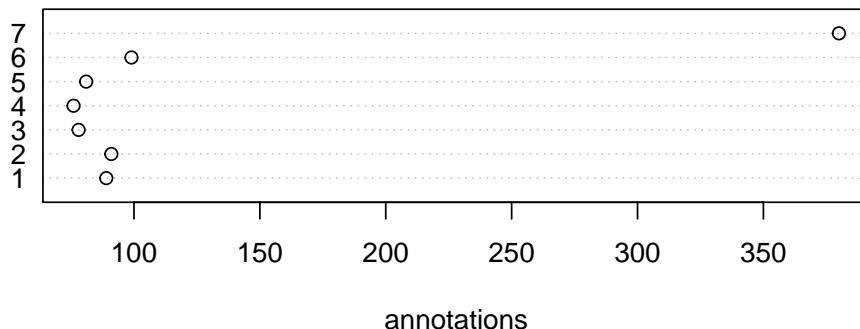
Simple exploratory analysis of annotations. First, make a collection.

```
> library(matR)
> IDs <- c("4441679.3", "4441680.3", "4441682.3", "4441695.3", "4441696.3", "4440463.3", "4440464.3")
> names(IDs) <- c("cow rumen (a)", "cow rumen (b)", "cow rumen (c)", "fish gut (a)", "fish gut (b)", "lean meat (a)", "lean meat (b)")
> cc <- collection(IDs)
```

Frequency of annotations in these seven samples.

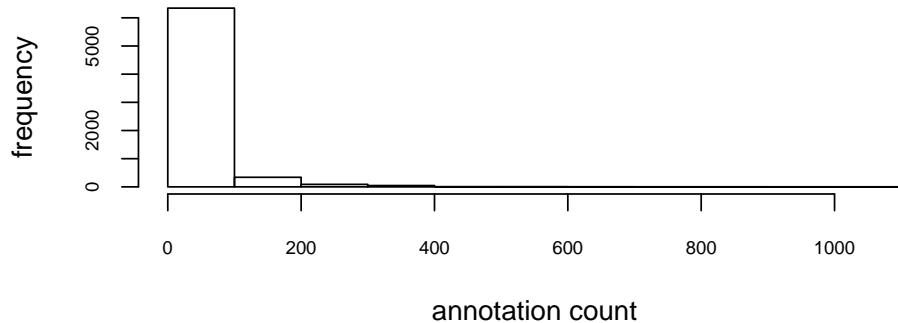
```
> n <- table(apply(cc$nsc, 1, Matrix::nnzero))
> dotchart(n, main=paste("occurrence of", sum(n), "annotations among seven samples"), xlab="annotations")
```

occurrence of 894 annotations among seven samples

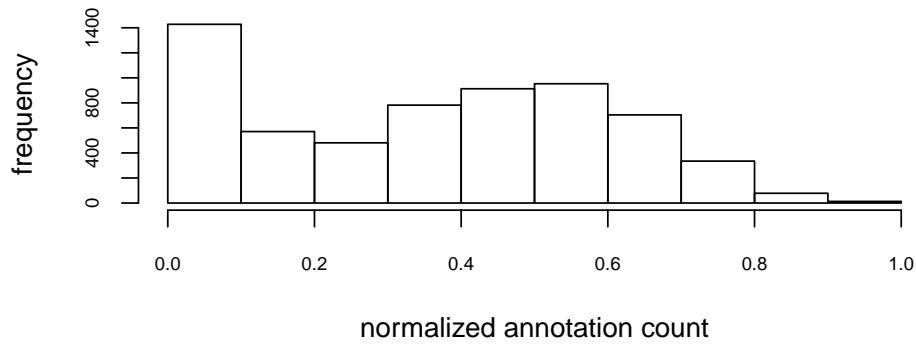


Histogram across seven samples of raw, then standardized, abundances.

```
> hist(cc$raw, main="", cex.axis=0.7, xlab="annotation count", ylab="frequency")
```



```
> hist(cc$nsn, main="", cex.axis=0.7, xlab="normalized annotation count", ylab="frequency")
```

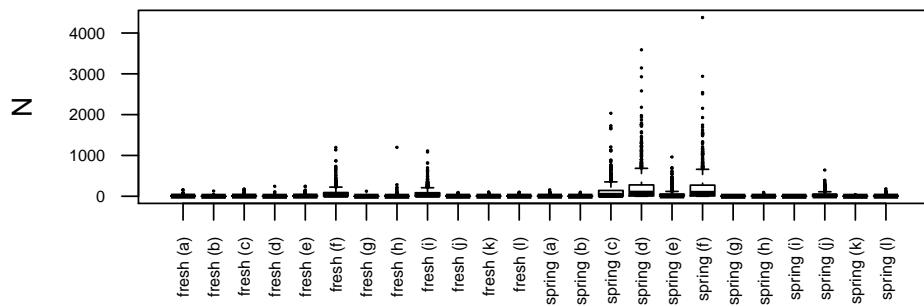


A new collection, and boxplots showing annotation of all samples.

```
> IDs <- c("4440424.3 4440423.3 4440439.3 4440422.3 4440412.3 4440414.3 4440440.3 4440413.3 4440411.3 4440410.3 4440409.3 4440408.3")
> cc <- collection(IDs)
> names(cc) <- c(paste("fresh (", letters [1:12], ")"), paste("spring (", letters [1:12], ")"), "all")
> names(cc)

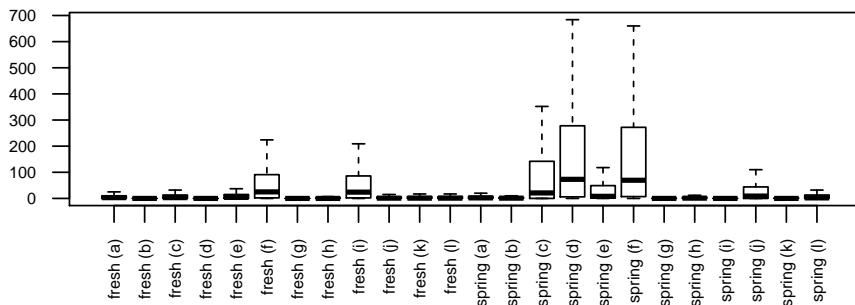
> boxplot(cc, view="raw", main="raw counts", names=names(cc), ylab="N", las=2, outcex=0.2, pch=20)
```

raw counts



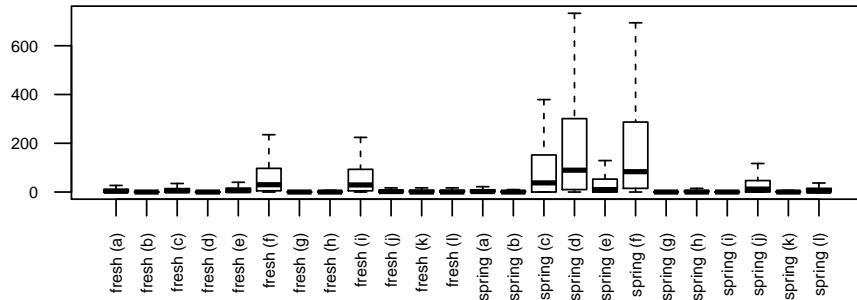
```
> boxplot(cc, view="raw", main="no outliers", names=names(cc), las=2, outcex=0.2, pch=20, outline=FALSE)
```

no outliers



```
> boxplot(cc, view="nsc", main="no outliers, no singletons", names=names(cc), las=2, outcex=0.2, pch=20)
```

no outliers, no singletons



```
> boxplot(cc, view="nsn", main="no singletons, normalized", names=names(cc), las=2, outcex=0.2, pch=20,
```

no singletons, normalized

